

In the Specification

Please amend the paragraph from page 25 to 26 as follows:

High seed coat peroxidase (*EpEp*) soybean cultivar Harosoy 63 plants were grown in field plots outdoors. Pods were harvested 35 days after flowering and seeds in the mid-to-late developmental stage were excised. The average fresh mass was 250 mg per seed. Seed coats were dissected and immediately frozen in liquid nitrogen. The frozen tissue was lyophilized and total RNA extracted in 100 mM Tris-HCl pH 9.0, 20 mM EDTA, 4% (w/v) sarkosyl, 200 mM NaCl, and 16 mM DTT, and precipitated with LiCl using the standard phenol/chloroform method described by Wang and Vodkin (1994). The poly(A)⁺ RNA was purified on oligo(dT) cellulose columns prior to cDNA synthesis, size selection, ligation into the λ ZAP Express vector, and packaging according to instructions (Stratagene). A degenerate oligonucleotide with the 5' to 3' sequence of TT(C/T)CA(C/T)GA(C/T)TG(C/T)TT(C/T)GT (SEQ ID NO:3) was 5' end labelled to high specific activity and used as a probe to isolate peroxidase cDNA clones (Sambrook *et al.*, 1989). Duplicate plaque lifts were made to nylon filters (Amersham), UV fixed, and prehybridized at 36°C for 3 h in 6 x SSC, 20 mM Na₂HPO₄ (pH6.8), 5 x Denhardt's, 0.4 % SDS, and 500 μ g/mL salmon sperm DNA. Hybridization was in the same buffer, without Denhardt's, at 36°C for 16 h. Filters were washed quickly with several changes of 6 x SSC and 0.1 % SDS, first at room

temperature and finally at 40°C, prior to autoradiography for 16 h at -70°C with an intensifying screen.

Please amend the paragraph from page 33 to 34 as follows:

Primers were designed from the DNA sequence to compare *EpEp* and *epep* genotypes by PCR analysis. Figure 6 shows PCR amplification products from four different primer combinations using OX312 (*epep*) and OX347 (*EpEp*) genomic DNA as template. The primer annealing site for prx29+ begins 182 bp upstream from the ATG start codon; the remaining primer sites are shown in Figure 1. Amplification with primers prx2+ and prx6-, and with prx12+ and prx10- produced the expected products of 1.9 kb and 860 bp, respectively, regardless of the *Ep/ep* genotype of the template DNA. However, PCR amplification with primers prx9+ and prx10-, and with prx29+ and prx10- generated the expected products only when template DNA was from plants carrying the dominant *Ep* allele. When template DNA was from an *epep* genotype, no product was detected using primers prx9+ and prx10- and a smaller product was amplified with primers prx29+ and prx10-. The products resulting from amplification of OX312 or OX347 template DNA with primers prx29+ and prx10- were directly sequenced and compared. The polymorphism is due to an 87 bp deletion occurring within this DNA fragment in OX312 plants, as shown in Figure 5 (corresponding to nucleotides 1524 to 1610 of SEQ ID NO:2). This deletion begins nine bp upstream from the translation start codon and includes 78 bp of sequence at the 5' end of the open reading frame, including the prx9+ primer annealing site.